



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 08/657,749C
Source: 1600
Date Processed by STIC: 8/18/2003

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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/657,749C

DATE: 08/18/2003

TIME: 13:10:45

Input Set : A:\1651802.app

Output Set: N:\CRF4\08182003\H657749C.raw

3 <110> APPLICANT: METZ, JAMES G.
 4 LARDIZABAL, KATHRYN D.
 5 LASSNER, MICHAEL
 7 <120> TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING A PLANT CYTOPLASMIC
 8 PROTEIN INVOLVED IN FATTY ACYL-COA METABOLISM
 10 <130> FILE REFERENCE: 16518.025
 12 <140> CURRENT APPLICATION NUMBER: 08/657,749C
 13 <141> CURRENT FILING DATE: 1996-05-30
 15 <150> PRIOR APPLICATION NUMBER: PCT/US94/13686
 16 <151> PRIOR FILING DATE: 1994-11-30
 18 <150> PRIOR APPLICATION NUMBER: 08/265,047
 19 <151> PRIOR FILING DATE: 1994-06-23
 21 <150> PRIOR APPLICATION NUMBER: 08/160,602
 22 <151> PRIOR FILING DATE: 1993-11-30
 24 <150> PRIOR APPLICATION NUMBER: 08/066,299
 25 <151> PRIOR FILING DATE: 1993-05-20
 27 <150> PRIOR APPLICATION NUMBER: PCT/US92/09863
 28 <151> PRIOR FILING DATE: 1992-11-13
 30 <150> PRIOR APPLICATION NUMBER: 07/933,411
 31 <151> PRIOR FILING DATE: 1992-08-21
 33 <150> PRIOR APPLICATION NUMBER: 07/796,256
 34 <151> PRIOR FILING DATE: 1991-11-20
 36 <160> NUMBER OF SEQ ID NOS: 53
 38 <170> SOFTWARE: PatentIn Ver. 2.1
 40 <210> SEQ ID NO: 1
 41 <211> LENGTH: 1786
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Simmondsia chinensis
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (80)..(1558)
 49 <220> FEATURE:
 50 <221> NAME/KEY: modified_base
 51 <222> LOCATION: (1537)
 52 <223> OTHER INFORMATION: a, c, t, or g
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 55 <221> NAME/KEY: modified_base
 56 <222> LOCATION: (1608)..(1609)
 57 <223> OTHER INFORMATION: a, c, t, or g
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 62 gtagcaaact taaaagaaa atg gag atg gga agc att tta gag ttt ctt 112
 63 Met Glu Met Gly Ser Ile Leu Glu Phe Leu

Does Not Comply
Corrected Diskette Needed

Pr 5-8

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DATE: 08/18/2003
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Input Set : A:\1651802.app
Output Set: N:\CRF4\08182003\H657749C.raw

64	1	5	10	
66	gat aac aaa gcc att ttg gtc act ggt gct act gtc tcc tta gca aaa	160		
67	Asp Asn Lys Ala Ile Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys			
68	15 20 25			
70	att ttt gtg gag aag gta ctg agg agt caa ccg aat gtg aag aaa ctc	208		
71	Ile Phe Val Glu Lys Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu			
72	30 35 40			
74	tat ctt ctt ttg aga gca acc gat gac gag aca gct gct cta cgc ttg	256		
75	Tyr Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu			
76	45 50 55			
78	caa aat gag gtt ttt gga aaa gag ttg ttc aaa gtt ctg aaa caa aat	304		
79	Gln Asn Glu Val Phe Gly Glu Leu Phe Lys Val Leu Lys Gln Asn			
80	60 65 70 75			
82	tta ggt gca aat ttc tat tcc ttt gta tca gaa aaa gtg act gta gta	352		
83	Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val			
84	80 85 90			
86	ccc ggt gat att act ggt gaa gac ttg tgc ctc aaa gac gtc aat ttg	400		
87	Pro Gly Asp Ile Thr Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu			
88	95 100 105			
90	aag gaa gaa atg tgg agg gaa atc gat gtt gtt gtc aat cta gct gct	448		
91	Lys Glu Glu Met Trp Arg Glu Ile Asp Val Val Asn Leu Ala Ala			
92	110 115 120			
94	aca atc aac ttc att gaa agg tac gac gtg tct ctg ctt atc aac aca	496		
95	Thr Ile Asn Phe Ile Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr			
96	125 130 135			
98	tat gga gcc aag tat gtt ttg gac ttc gcg aag aag tgc aac aaa tta	544		
99	Tyr Gly Ala Lys Tyr Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu			
100	140 145 150 155			
102	aag ata ttt gtt cat gta tct act gct tat gta tct gga gag aaa aat	592		
103	Lys Ile Phe Val His Val Ser Thr Ala Tyr Val Ser Gly Glu Lys Asn			
104	160 165 170			
106	ggg tta ata ctg gag aag cct tat tat atg ggc gag tca ctt aat gga	640		
107	Gly Leu Ile Leu Glu Lys Pro Tyr Tyr Met Gly Glu Ser Leu Asn Gly			
108	175 180 185			
110	aga tta ggt ctg gac att aat gta gag aag aaa ctt gtg gag gca aaa	688		
111	Arg Leu Gly Leu Asp Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys			
112	190 195 200			
114	atc aat gaa ctt caa gca gcg ggg gca acg gaa aag tcc att aaa tcg	736		
115	Ile Asn Glu Leu Gln Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser			
116	205 210 215			
118	aca atg aag gac atg ggc atc gag agg gca aga cac tgg gga tgg cca	784		
119	Thr Met Lys Asp Met Gly Ile Glu Arg Ala Arg His Trp Gly Trp Pro			
120	220 225 230 235			
122	aat gtg tat gta ttc acc aag gca tta ggg gag atg ctt ttg atg caa	832		
123	Asn Val Tyr Val Phe Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln			
124	240 245 250			
126	tac aaa ggg gac att ccg ctt act att att cgt ccc acc atc atc acc	880		
127	Tyr Lys Gly Asp Ile Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr			
128	255 260 265			

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130	agc act ttt aaa gag ccc ttt cct ggt tgg gtt gaa ggt gtc agg acc	928
131	Ser Thr Phe Lys Glu Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr	
132	270 275 280	
134	atc gat aat gta cct gta tat tat ggt aaa ggg aga ttg agg tgt atg	976
135	Ile Asp Asn Val Pro Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met	
136	285 290 295	
138	ctt tgc gga ccc agc aca ata att gac ctg ata ccg gca gat atg gtc	1024
139	Leu Cys Gly Pro Ser Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val	
140	300 305 310 315	
142	gtg aat gca acg ata gta gcc atg gtg gcg cac gca aac caa aga tac	1072
143	Val Asn Ala Thr Ile Val Ala Met Val Ala His Ala Asn Gln Arg Tyr	
144	320 325 330	
146	gta gag ccg gtg aca tac cat gtg gga tct tca gcg gcg aat cca atg	1120
147	Val Glu Pro Val Thr Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met	
148	335 340 345	
150	aaa ctg agt gca tta cca gag atg gca cac cgt tac ttc acc aag aat	1168
151	Lys Leu Ser Ala Leu Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn	
152	350 355 360	
154	cca tgg atc aac ccg gat cgc aac cca gta cat gtg ggt cgg gct atg	1216
155	Pro Trp Ile Asn Pro Asp Arg Asn Pro Val His Val Gly Arg Ala Met	
156	365 370 375	
158	gtc ttc tcc tcc ttc acc ttc cac ctt tat ctc acc ctt aat ttc	1264
159	Val Phe Ser Ser Phe Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe	
160	380 385 390 395	
162	ctc ctt cct ttg aag gta ctg gag ata gca aat aca ata ttc tgc caa	1312
163	Leu Leu Pro Leu Lys Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln	
164	400 405 410	
166	tgg ttc aag ggt aag tac atg gat ctt aaa agg aag acg agg ttg ttg	1360
167	Trp Phe Lys Gly Lys Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu	
168	415 420 425	
170	ttg cgt tta gta gac att tat aaa ccc tac ctc ttc ttc caa ggc atc	1408
171	Leu Arg Leu Val Asp Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile	
172	430 435 440	
174	ttt gat gac atg aac act gag aag ttg cgg att gct gca aaa gaa agc	1456
175	Phe Asp Asp Met Asn Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser	
176	445 450 455	
178	ata gtt gaa gct gat atg ttt tac ttt gat ccc agg gca att aac tgg	1504
179	Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp	
180	460 465 470 475	
W--> 182	gaa gat tac ttc ttg aaa act cat ttc cca ggn gtc gta gag cac gtt	1552
183	Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val	
184	480 485 490	
186	ctt aac taaaagttac ggtacgaaaa tgagaagatt ggaatgcatt caccgaaagn	1608
187	Leu Asn	
189	ncaacataaa agacgtggtt aaagtcatgg tcaaaaaaga aataaaatgc agttaggttt	1668
191	gtgttgcagt tttgattctt ttttattttt cttgtacttt tgatctttt ctttttaat	1728
193	gaaatttctc tctttgtttt gtaaaaaaaaaaaaa gagctcctgc agaagctt	1786
196	<210> SEQ ID NO: 2	
197	<211> LENGTH: 493	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/657,749C

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Input Set : A:\1651802.app
Output Set: N:\CRF4\08182003\H657749C.raw

198 <212> TYPE: PRT
199 <213> ORGANISM: Simmondsia chinensis
201 <400> SEQUENCE: 2
202 Met Glu Met Gly Ser Ile Leu Glu Phe Leu Asp Asn Lys Ala Ile
203 1 5 10 15
205 Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys Ile Phe Val Glu Lys
206 20 25 30
208 Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu Tyr Leu Leu Arg
209 35 40 45
211 Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu Gln Asn Glu Val Phe
212 50 55 60
214 Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn Leu Gly Ala Asn Phe
215 65 70 75 80
217 Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val Pro Gly Asp Ile Thr
218 85 90 95
220 Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu Lys Glu Glu Met Trp
221 100 105 110
223 Arg Glu Ile Asp Val Val Asn Leu Ala Ala Thr Ile Asn Phe Ile
224 115 120 125
226 Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr Tyr Gly Ala Lys Tyr
227 130 135 140
229 Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu Lys Ile Phe Val His
230 145 150 155 160
232 Val Ser Thr Ala Tyr Val Ser Gly Glu Lys Asn Gly Leu Ile Leu Glu
233 165 170 175
235 Lys Pro Tyr Tyr Met Gly Glu Ser Leu Asn Gly Arg Leu Gly Leu Asp
236 180 185 190
238 Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys Ile Asn Glu Leu Gln
239 195 200 205
241 Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser Thr Met Lys Asp Met
242 210 215 220
244 Gly Ile Glu Arg Ala Arg His Trp Gly Trp Pro Asn Val Tyr Val Phe
245 225 230 235 240
247 Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln Tyr Lys Gly Asp Ile
248 245 250 255
250 Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr Ser Thr Phe Lys Glu
251 260 265 270
253 Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr Ile Asp Asn Val Pro
254 275 280 285
256 Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met Leu Cys Gly Pro Ser
257 290 295 300
259 Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val Val Asn Ala Thr Ile
260 305 310 315 320
262 Val Ala Met Val Ala His Ala Asn Gln Arg Tyr Val Glu Pro Val Thr
263 325 330 335
265 Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met Lys Leu Ser Ala Leu
266 340 345 350
268 Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn Pro Trp Ile Asn Pro
269 355 360 365

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Input Set : A:\1651802.app
Output Set: N:\CRF4\08182003\H657749C.raw

271 Asp Arg Asn Pro Val His Val Gly Arg Ala Met Val Phe Ser Ser Phe
272 370 375 380
274 Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe Leu Leu Pro Leu Lys
275 385 390 395 400
277 Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln Trp Phe Lys Gly Lys
278 405 410 415
280 Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu Leu Arg Leu Val Asp
281 420 425 430
283 Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile Phe Asp Asp Met Asn
284 435 440 445
286 Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser Ile Val Glu Ala Asp
287 450 455 460
289 Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp Glu Asp Tyr Phe Leu
290 465 470 475 480
292 Lys Thr His Phe Pro Gly Val Val Glu His Val Leu Asn
293 485 490

297 <210> SEQ ID NO: 3

298 <211> LENGTH: 1733

299 <212> TYPE: DNA

300 <213> ORGANISM: Simmondsia chinensis

302 <220> FEATURE:

303 <221> NAME/KEY: CDS

304 <222> LOCATION: (39)..(1610)

306 <220> FEATURE:

307 <221> NAME/KEY: modified_base

308 <222> LOCATION: (676)

309 <223> OTHER INFORMATION: a, c, t, or g

311 <400> SEQUENCE: 3

312 ggaactccat cccttcctcc ctcactccctc tctctaca atg aag gcc aaa aca atc 56
313 Met Lys Ala Lys Thr Ile

what about "n" at location 737?

(see p 6)

314 1 5
316 aca aac ccg gag atc caa gtc tcc acg acc atg acc acc acg acc acg 104
317 Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr
318 10 15 20
320 act atg acc gcc act ctc ccc aac ttc aag tcc tcc atc aac tta cac 152
321 Thr Met Thr Ala Thr Leu Pro Asn Phe Lys Ser Ser Ile Asn Leu His
322 25 30 35
324 cac gtc aag ctc ggc tac cac tac tta atc tcc aat gcc ctc ttc ctc 200
325 His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn Ala Leu Phe Leu
326 40 45 50
328 gta ttc atc ccc ctt ttg ggc ctc gct tcg gcc cat ctc tcc ttc 248
329 Val Phe Ile Pro Leu Leu Gly Leu Ala Ser Ala His Leu Ser Ser Phe
330 55 60 65 70
332 tcg gcc cat gac ttg tcc ctg ctc ttc gac ctc ctt cgc cgc aac ctc 296
333 Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu Arg Arg Asn Leu
334 75 80 85
336 ctc cct gtt gtc gtt tgt tct ttc ctc ttc gtt tta tta gca acc cta 344
337 Leu Pro Val Val Cys Ser Phe Leu Phe Val Leu Leu Ala Thr Leu
338 90 95 100

08/657,749C 6

agc ttg ttt aac cca acg ccg tcg tca tcc atg ata gtt aac cat 728
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ser Met Ile Val Asn His
215 220 225 230
h location 20 tac aag ctn agg ggt aat ata ctt agc tat aat ctt ggt ggc atg ggt 776
Tyr Lys Xaa Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly
235 240 245

see p. 7 for more more

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<210> SEQ ID NO 4
<211> LENGTH: 524
<212> TYPE: PRT
<213> ORGANISM: Simmondsia chinensis
<220> FEATURE:
<221> NAME/KEY: MOD_RES *what about Xaa at location 233?*
<222> LOCATION: (213)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 4

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1 5 10 15
Met Thr Thr Thr Thr Thr Met Thr Ala Thr Leu Pro Asn Phe Lys
20 25 30
Ser Ser Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile
35 40 45
Ser Asn Ala Leu Phe Leu Val Phe Ile Pro Leu Leu Gly Leu Ala Ser
50 55 60
Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp
65 70 75 80
Leu Leu Arg Arg Asn Leu Leu Pro Val Val Val Cys Ser Phe Leu Phe
85 90 95
Val Leu Leu Ala Thr Leu His Phe Leu Thr Arg Pro Arg Asn Val Tyr
100 105 110
Leu Val Asp Phe Gly Cys Tyr Lys Pro Gln Pro Asn Leu Met Thr Ser
115 120 125
His Glu Met Phe Met Asp Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys
130 135 140
Glu Asn Ile Glu Phe Gln Arg Lys Ile Leu Glu Arg Ala Gly Met Gly
145 150 155 160
Arg Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Val Pro Ala Glu Pro
165 170 175
Ser Ile Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala
180 185 190
Ile Asp Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly
195 200 205
Ile Leu Val Val Xaa Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser
210 215 220
Ser Met Ile Val Asn His Tyr Lys Xaa Arg Gly Asn Ile Leu Ser Tyr
225 230 235 240



T

see p.8

8
RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/08/657,749C

DATE: 08/18/2003
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Input Set : A:\1651802.app
Output Set: N:\CRF4\08182003\H657749C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1537,1608,1609
Seq#:3; N Pos. 676,737
Seq#:3; Xaa Pos. 213,233
Seq#:4; Xaa Pos. 213,233
Seq#:22; N Pos. 345
Seq#:22; Xaa Pos. 102
Seq#:23; Xaa Pos. 102
Seq#:24; N Pos. 155,217
Seq#:24; Xaa Pos. 51,72
Seq#:25; Xaa Pos. 51,72
Seq#:31; Xaa Pos. 3,10
Seq#:35; Xaa Pos. 4,5
Seq#:36; Xaa Pos. 7,8,11
Seq#:38; Xaa Pos. 1,17
Seq#:39; Xaa Pos. 7
Seq#:42; N Pos. 9,12,15
Seq#:43; N Pos. 15
Seq#:46; Xaa Pos. 3
Seq#:47; N Pos. 30,33
Seq#:49; N Pos. 30,33,36
Seq#:50; N Pos. 29,32,35
Seq#:52; N Pos. 39
Seq#:53; N Pos. 27

*Please ensure these n/Xaa
locations are explained*